

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:55:09 ; Search time 194 Seconds
(without alignments)
625.794 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGGQGFPRQECGEALP.....LVVLGVLLGQFVWRPFKS 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	1 BAK_HUMAN	Q16611 homo sapien
2	1103	100.0	211	2 CAG33700	Cag33700 homo sapi
3	1075	97.5	211	1 BAK2_HUMAN	Q13014 homo sapien
4	977.5	88.6	210	2 O6NF33	O6nf33 homo sapien
5	845	76.6	209	2 O8C264	O8c264 mus musculus
6	839	76.1	209	2 O9JX59	O9jx59 rattus norv
7	829.5	75.2	208	1 BAK_MOUSE	O08734 mus musculus
8	733	66.5	163	2 O9MZS6	O9mzs6 ovis aries
9	452	41.0	151	2 O91WX5	O91wx5 mus musculus
10	452	41.0	151	2 AAH57589	Aah57589 mus muscu
11	390	35.4	80	2 O77738	O77738 sus scrofa
12	189	17.1	239	1 BCL2_HUMAN	P10415 homo sapien
13	186	16.9	239	1 BCL2_BOVIN	O02718 bos taurus
14	184	16.7	239	1 BCLX_CHICK	Q00709 gallus gall
15	183.5	16.6	233	1 BCLX_CHICK	O9w6f1 gallus gall
16	181	16.4	211	2 O9W6F1	O9w6f1 gallus gall
17	181	16.4	217	2 O99N35	O99n35 mus musculus
18	181	16.4	233	1 BCLX_MOUSE	O64373 mus musculus
19	181	16.4	233	1 BCLX_RAT	P53563 rattus norv
20	181	16.4	233	2 O9MTW4	O9mtw4 oryctolagus
21	180.5	16.4	199	2 O8C5P0	O8c5p0 mus musculus
22	180	16.3	201	2 O6GI15	O6gi15 xenopus tro
23	180	16.3	233	1 BCLX_HUMAN	O07817 homo sapien
24	180	16.3	233	2 O76LT7	O76lt7 canis fam
25	180	16.3	233	2 O9MZS7	O9mzs7 ovis aries
26	180	16.3	233	2 O8SQ42	O8sq42 felis silve
27	180	16.3	233	2 BAB71819	Bab71819 canis fam
28	180	16.3	233	2 AAP35872	Aap35872 homo sapi
29	180	16.3	239	2 Q75SV7	Q75sv7 canis fam
30	180	16.3	239	2 BAD05044	Bad05044 canis fam
31	179.5	16.3	236	1 BCL2_MOUSE	P10417 mus musculus

ALIGNMENTS

RESULT 1

BAK_HUMAN	STANDARD;	PRT;	211 AA.
ID	BAK_HUMAN		
AC	Q16611; Q92533;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-OCT-2004 (Rel. 45, Last annotation update)		
DE	Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK) (BCL2-like 7 protein).		
GN	Name=BAK1; Synonyms=BAK, BCL2L7;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=B-cell;		
RX	MEDLINE=95231652; PubMed=7715729;		
RA	Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,		
RA	Grinham C.J., Martinou J.C., Brown R.;		
RT	"Cloning of a bcl-2 homologue by interaction with adenovirus E1B		
RT	19K.";		
RL	Nature 374:731-733 (1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95231653; PubMed=7715730;		
RA	Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,		
RA	Evan G.I., Guild B.C.;		
RT	"Induction of apoptosis by the Bcl-2 homologue Bak.";		
RL	Nature 374:733-736 (1995).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95231654; PubMed=7715731;		
RA	Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,		
RA	Tomei L.D., Barr P.J.;		
RT	"Modulation of apoptosis by the widely distributed Bcl-2 homologue		
RT	Bak.";		
RL	Nature 374:736-739 (1995).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;		
RA	Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,		
RA	Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,		
RA	Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,		
RA	Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,		
RA	Babbage A.K., Baggeley C.L., Bailey J., Banerjee R., Barker D.J.,		

32	178.5	16.2	236	1	BCL2_RAT
33	177.5	16.1	236	2	Q7TSN8
34	177.5	16.1	236	2	Q8BQK4
35	177.5	16.1	236	2	Q923R6
36	177	16.0	233	2	Q9N1A2
37	176.5	16.0	199	2	Q6NTH7
38	176.5	16.0	199	2	Aah68988
39	176	16.0	180	2	Q8BDD5
40	176	16.0	193	1	BCLW_HUMAN
41	176	16.0	233	1	BCLX_PIG
42	175	15.9	235	2	Q8I008
43	174	15.8	180	2	Q9BDX7
44	173.5	15.7	236	2	O6R755
45	173.5	15.7	236	2	AAR92491

P49950	rattus norv
Q7tsn8	rattus norv
Q8bqk4	mus musculus
Q923r6	cricetus
Q9n1a2	sus scrofa
Q6nth7	mus musculus
Aah68988	mus muscu
Q8bdd5	bos taurus
Q8bdk7	bos taurus
Q8i008	felis silve
Q9bdx7	bos taurus
O6r755	canis fam
Aar92491	canis fam

RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Culler K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gibby L.M., Gilson C.J., Githero R.J., Graham D.V., Grant M.,
RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Hallis K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maslen G.L., Matthews L., McCann C.T., McLaren S.J., McLay K.,
RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA Schra H.K., Sheridan B., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA Theaker A.G., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.,
RT "The DNA sequence and analysis of human chromosome 6.",
RL Nature 425:805-811(2003).
[6]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins P.S., Wagner L., Grouse L.H., Derge J.G.,
RA Klausner R.D., Feingold E.A., Grouse L.H., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavini T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RN SEQUENCE OF 96-206 FROM N.A.
RP SEQUENCE OF 96-206 FROM N.A.
RA Eguchi H., Hayashi S.;
RT "Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and
Bak, as well as susceptibility to therapeutic agents of human breast
cancer cells.",
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[8]
RN MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell
death and protein binding functions.",
RL EMBO J. 14:5589-5596(1995).
[9]
RN STRUCTURE BY NMR OF 72-87.
RX MEDLINE=97172562; PubMed=9020082;
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,

RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Feick S.W.;
RT "Structure of Bcl-xL-Bak peptide complex: recognition between
regulators of apoptosis.",
RL Science 275:983-986(1997).
CC -1- FUNCTION: In the presence of an appropriate stimulus, accelerates
programmed cell death by binding to, and antagonizing the a
repressor Bcl-2 or its adenovirus homolog E1B 19K protein.
CC -1- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19K protein, and Bcl-
X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with
highest levels in the heart and skeletal muscle.
CC -1- DOMAIN: Inactive BH3 domain is required by BIK, BID, BAK, BAD and
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family.
CC -1- SIMILARITY: Belongs to the Bcl-2 family.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
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CC
CC EMBL; X84213; CAA58997.1; -;
CC EMBL; U23765; AAA33066.1; -;
CC EMBL; U16811; AAA74466.1; -;
CC EMBL; AY260471; AAC74828.1; -;
CC EMBL; Z93017; CAB56526.1; -;
CC EMBL; BC004431; AAH04431.1; -;
CC EMBL; D88397; BAA13606.1; -;
CC EMBL; D88396; BAA13606.1; JOINED.
CC PIR; S58873; S58873.
CC PDB; 1BXL; NMR; B=72-87.
CC Genew; HGNC:949; BAK1.
CC MIM; 600516; -;
CC GO; GO:0008637; P.apoptotic mitochondrial changes; TAS.
CC InterPro; IPR00712; BCL2_BH.
CC InterPro; IPR002475; BCL2_family.
CC Pfam; PF00452; Bcl-2; 1.
CC PROSITE; PS00662; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC 3D-structure; Apoptosis; Polymorphism; Transmembrane.
FT DOMAIN 74 88
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 Potential.
FT VARIANT 28 28 A -> V.
FT VARIANT 69 69 /FTID=VAR_018829.
FT TURN 74 75 /FTIG=VAR_018930.
FT HELIX 76 84
FT TURN 85 85
SQ SEQUENCE 211 AA; 23409 MW; A2200FE72A46D04E CRC64;

Query Match 100.0%; Score 1103; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.4e-90;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGQGGPPROECGEPALPSASEEQVAQDTEVFRSVYFVRHQCEAEGVAAPADPEM 60
|||||
DB 1 MASGGQGGPPROECGEPALPSASEEQVAQDTEVFRSVYFVRHQCEAEGVAAPADPEM 60
|||||

QY 61 VTLPDPSMTGQVGRQLAIIIGDDINRRYDSFQTMLOHQTAEVAYEYFKIATSLPE 120
|||||

Db 61 VTLPQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180
QY 181 LNLNGSPILNLVVLGVLLGQFVWRFFKS 211
Db 181 LNLNGSPILNLVVLGVLLGQFVWRFFKS 211

RESULT 2
ID CAG33700 PRELIMINARY; PRT; 211 AA.
AC CAG33700; (Created)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 01-JUN-2004 (TREMBlrel. 27, Last sequence update)
DE 01-JUN-2004 (TREMBlrel. 27, Last annotation update)
DE BAK1 protein.
GN BAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP "Cloning of human full open reading frames in Gateway(TM) system entry
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT vector (pDONR201)";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR457419; CAG33700.1; -. A2200FE72A46D04E CRC64;
SQ SEQUENCE 211 AA; 23409 MW; 23409 MW; 703875EC4DCC1D3 CRC64;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 4.4e-90;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGQPGPPRCGEGEPALPSASEEQVAQDTEEVFRSVYFVRHQEQEAEAGVAAADPEM 60
Db 1 MASGGQPGPPRCGEGEPALPSASEEQVAQDTEEVFRSVYFVRHQEQEAEAGVAAADPEM 60

QY 61 VTLPQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
Db 61 VTLPQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180

RESULT 3
ID BAK2 HUMAN STANDARD; PRT; 211 AA.
AC Q13014;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator
DE BAK-2).
GN Name=BCL2L7P1; Synonyms=BAK2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95231654; PubMed=7715731;
RX Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
RA Tomei L.D., Barr P.J.;

RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
Bak.";
RL Nature 374:736-739(1995).
CC -!- FUNCTION: In the presence of an appropriate stimulus, accelerates
programmed cell death by binding to, and antagonizing the a
repressor Bcl-2 or its adenovirus homolog E1B 19k protein.
CC -!- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-
X(L).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with
highest levels in the heart and skeletal muscle.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
BAX for their pro-apoptotic activity and for their interaction
with anti-apoptotic members of the Bcl-2 family. Apoptotic members
of the Bcl-2 family.
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- CAUTION: This is probably the product of a pseudogene.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U16812; AAA74467.1; -.
DR PIR; S58875; S58875.
DR HSSP; Q16611; 1BXL.
DR Genew; HGNC:996; BCL2L7P1.
DR GO; GO:0016020; C:membrane; NAS.
DR GO; GO:0006917; P:induction of apoptosis; NAS.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF0452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
KW Apoptosis; Hypothetical protein; Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205 Potential.
SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCC1D3 CRC64;

Query Match 97.5%; Score 1075; DB 1; Length 211;
Best Local Similarity 97.2%; Pred. No. 1.4e-87;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGQPGPPRCGEGEPALPSASEEQVAQDTEEVFRSVYFVRHQEQEAEAGVAAADPEM 60
Db 1 MASGGQPGPPRCGEGEPALPSASEEQVAQDTEEVFRSVYFVRHQEQEAEAGVAAADPEM 60

QY 61 VTLPQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120
Db 61 VTLPQSSSTMGOVGRQLAIGDDINRRYDSEFQTMQLHLOPTAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180
Db 121 SGINWGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVDFMLHHCIAEWIAQRGGWAA 180

QY 181 LNLNGSPILNLVVLGVLLGQFVWRFFKS 211
Db 181 LNLNGSPILNLVVLGVLLGQFVWRFFKS 211

RESULT 4
Q9NFF3

```

ID Q8NFF3 PRELIMINARY; PRT; 190 AA.
AC Q8NFF3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pro-apoptotic protein BAKN variant.
GN Name=BAK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Ma J.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205090; AAM74949.1; -.
DR HSP; Q16611; 1BX1.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR000712; BCL2_family.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 190 AA; 21231 MW; A9D4EB8526D0897B CRC64;

Query Match 88.6%; Score 977.5; DB 2; Length 190;
Best Local Similarity 90.0%; Pred. No. 5.9e-79;
Matches 190; Conservative 0; Mismatches 0; Indels 21; Gaps 1;

QY 1 MASGGGPGPRQCEGPEALPSASEEQVAODTEVERSVYVYFHQEQEAGVAAPADPEM 60
DB 1 MASGGGPGPRQCEGPEALPSASEEQVAODTEVERSVYVYFHQEQEAGVAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 45 ----QPSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 99

QY 121 SGINGRVVALGFGYRLALHYQHGLTGLQVTRFVVDPMHLHICARWIAORGGWAA 180
DB 100 SGINGRVVALGFGYRLALHYQHGLTGLQVTRFVVDPMHLHICARWIAORGGWAA 159

QY 181 LNLGNPILNLVLGLVGLLQGVVRRFPKS 211
DB 160 LNLGNPILNLVLGLVGLLQGVVRRFPKS 190

RESULT 5
Q8C264 PRELIMINARY; PRT; 209 AA.
AC Q8C264;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone:F63004J23 product:BCL2-
DE antagonist/killer 1, full insert sequence.
GN Name=Bak1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Carninci P.;
RL MEDLINE=99279253; PubMed=10349636;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
SEQUENCE FROM N.A.

RC STRAIN=NOD;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoaka S.; Sasaki N.; Carninci P.;
RA Konno H.; Akiyama J.; Nishi K.; Kitsuai T.; Tashiro H.; Itoh M.;
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA Fujiwara S.; Inoue K.; Ozawa Y.; Izawa M.; Ohara E.; Watahiki M.;
RA Yoneda Y.; Ishikawa T.; Tanaka T.; Matsuura S.; Kawai J.;
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.;
RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hiraoka T.; Hirozane T.;
RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.;
RA Katoh H.; Kawai J.; Kojima Y.; Kondo S.; Konno H.; Kouda M.; Koya S.;
RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohsato N.; Okazaki Y.;
RA Saito R.; Saitoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
RA Sasaki D.; Shibata K.; Shingawa A.; Shiraki T.; Sogabe Y.; Tagami M.;
RA Tsgawa A.; Takahashi F.; Takaku-Akanira S.; Takeda Y.; Tanaka T.;
RA Tomaru A.; Toya T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089220; BAC40796.1; -.
DR HSP; Q16611; 1BX1.
DR M3D; MG1:1057161; Bak1.
DR GO; GO:0008635; P:caspace activation via cytochrome c; IMP.
DR InterPro; IPR000712; BCL2_family.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA; 23234 MW; 55E72D29A8AFD18 CRC64;

Query Match 76.6%; Score 845; DB 2; Length 209;
Best Local Similarity 76.8%; Pred. No. 4.3e-67;
Matches 162; Conservative 21; Mismatches 26; Indels 2; Gaps 1;

QY 1 MASGGGPGPRQCEGPEALPSASEEQVAODTEVERSVYVYFHQEQEAGVAAPADPEM 60
DB 1 MASGGGPGPRQCEGPEALPSASEEQVAODTEVERSVYVYFHQEQEAGVAAPADPEM 58

QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSFQTMQLQLOPTAENAYEYFTKIATSLFE 120
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Db 59 DNLPLEPNSILGQVGRQLALIGDDINRRYDTFQNLLEQLQPTAGNAYELFTKIASSLFK 118
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 119 SGISWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 178
Qy 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Db 179 LSLRRDPILSVVIFGVLLGQFVVRFFRS 209

RESULT 6
Q9JK59 PRELIMINARY; PRT; 209 AA.
AC Q9JK59
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22672518; PubMed=12787069;
RA Itch T., Itch A., Pleasure D.;
RT "Bcl-2-related protein family gene expression during oligodendroglial
RT differentiation."
RL J. Neurochem. 85:1500-1512(2003).
DR EMBL; AF259504; AAF71760.1; -.
DR HSP; Q16611; IBLX.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR007112; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL_1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; UNKNOWN_1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA; 23153 MW; 2493B814B1972421-CRC64;

Query Match 76.18; Score 839; DB 2; Length 209;
Best Local Similarity 77.34; Pred. No. 1.5e-66;
Matches 163; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MASQGGPPRQECGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPADPEM 60
Db 1 MASQGGPPKPGDCDE-AL-SASEQQAQDTEEVFRSYVFRHQEQAEQVAAAPANPEM 58
Qy 61 VTLPQSSWTGQVGRQLALIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
Db 59 DNLPLEPNSILGQVGRQLALIGDDINRRYDTEFQNLLEQLQPTAGNAYELFTKIASSLFK 118
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 119 SGISWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 178
Qy 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Db 179 LSLRRDPILSVVIFGVLLGQFVVRFFRS 209

RESULT 7
BAK_MOUSE
ID BAK_MOUSE STANDARD; PRT; 208 AA.
AC O08734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

```
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
GN Name=Bak1; Synonyms=Bak;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Liver;
RX MEDLINE=97446138; PubMed=9299236;
RA Ulrich E., Kauffmann-Zen A., Hueber A.O., Williamson J.,
RA Chittenden T., Ma A., Evan G.I.;
RT "Gene structure, cDNA sequence, and expression of murine Bak, a
RT proapoptotic Bcl-2 family member."
RL Genomics 44:195-200(1997).
CC -!- FUNCTION: In the presence of an appropriate stimulus, accelerates
CC programmed cell death by binding to, and antagonizing the a
CC repressor Bcl-2 or its adenovirus homolog E1B 19k protein (By
CC similarity).
CC -!- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k protein, and Bcl-
CC X(L) (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family (By similarity).
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y13231; CAA73884.1; -.
CC HSP; Q16611; IBLX.
CC MGD; MGI:1097161; Bak1.
CC GO; GO:0008635; P:caspase activation via cytochrome c; IMP.
CC InterPro; IPR007112; Bcl2_BH.
CC InterPro; IPR002475; BCL2_FAMILY; 1.
CC Pfam; PF00452; Bcl-2; 1.
CC PROSITE; PS00062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC Apoptosis; Transmembrane.
CC DOMAIN 71 85 BH3.
CC DOMAIN 114 133 BH1.
CC DOMAIN 166 181 BH2.
CC TRANSMEM 185 202 Potential.
CC SEQUENCE 208 AA; 23300 MW; DAFCL1B160C523C9-CRC64;

Query Match 75.24; Score 829.5; DB 1; Length 208;
Best Local Similarity 76.34; Pred. No. 1e-65;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

Qy 1 MASQGGPPRQECGEPALPSASEEQVAQDTEEVFRSYVFRHQEQAEQVAAAPADPEM 60
Db 1 MASQGGPPKPGVGDDES--PSPSEQQAQDTEEVFRSYVFRHQEQAEQVAAAPANPEM 57
Qy 61 VTLPQSSWTGQVGRQLALIGDDINRRYDSEFQTMLOHLOPTAENAYEFTKIATSLFE 120
Db 58 DNLPLEPNSILGQVGRQLALIGDDINRRYDTEFQNLLEQLQPTAGNAYELFTKIASSLFK 117
Qy 121 SGINWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 180
Db 118 SGISWGRVALLGFGYRLALHYVQGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWAA 177
```


RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
[2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC STRAIN=CS7BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057589; AAH57589.1; -. 18C13BPF86E4F33B CRC64;
SQ SEQUENCE 151 AA; 16402 MW; 18C13BPF86E4F33B CRC64;

Query Match 41.0%; Score 452; DB 2; Length 151;
Best Local Similarity 75.0%; Pred. No. 3e-32;
Matches 87; Conservative 12; Mismatches 15; Indels 2; Gaps 1;

QY 1 MASGQGGPPRQCGEPALPSAEEQVAQDTEVFYSYVYRHCQEQEAGVAAADPDM 60
Db 1 MASGQGGPPKVGCDRES--PSPSEQVAQDTEVFYSYVYRHCQEQEAGVAAADPDM 58

QY 61 VTLPSPSTMGVQGRQLAIGDDINRRYDTEFQTLQHLQPTAENAYEFTKIAT 116
Db 59 DNLPLEPNSILGQVGRQLAIGDDINRRYDTEFQTLQHLQPTAENAYEFTKIAT 114

RESULT 11
077738
ID 077738 PRELIMINARY; PRT; 80 AA.
AC 077738
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Bak protein (Fragment).
GN Name=bak;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001204; CAA04598.1; -.
DR GO; GO:0042981; P:regulation of apoptosis; IIA.
DR InterPro; IPR000712; Bcl2 BH
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SW00337; BCL; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 8818 MW; FDLA983BD7D59C86 CRC64;

Query Match 35.4%; Score 390; DB 2; Length 80;
Best Local Similarity 92.5%; Pred. No. 4.4e-27;
Matches 74; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 50 EGVAAAPADPEMVTLPQPSSTMGVQGRQLAIGDDINRRYDTEFQTLQHLQPTAENAYE 109
Db 1 DGAAPAPDPEMVTLPQPSSTMGVQGRQLAIGDDINRRYDTEFQTLQHLQPTAENAYE 60

QY 110 YFTKIATSLFESGINWGRV 129
Db 61 YFTKIATSLFESGINWGRV 80

RESULT 12
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q13842; Q16197;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN Name=BCL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma";
Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo";
Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation";
Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma";
EMBO J. 7:1123-131(1988).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schachwitz W.S., Sherwood J.K., Witak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)";
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Testis;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RC SEQUENCE FROM N.A. (ISOFORM LONG).
RX STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilgerea X.; Mezquita C.; Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken spermatogenesis.";
RL Mcl. Reprod. Dev. 47:26-29(1997).
CC -!- FUNCTION: Dominant regulator of apoptotic cell death. The long form displays cell death repressor activity, whereas the short isoform promotes apoptosis (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC isoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC isoId=Q07816-2; Sequence=VSP_000514;
CC -!- TISSUE SPECIFICITY: Highest expression in organs with lymphoid development.
CC -!- DOMAIN: BH4 domain seems to be involved in the anti-apoptotic function. Intact BH1 and BH2 domains are required for anti-apoptotic activity (By similarity).
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
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CC -----
DR EMBL; Z23110; CAA80657.1; -;
DR EMBL; U26645; AAB07677.1; -;
DR PIR; A47537; A47537.
DR HSSP; P53563; 1AF3.
DR InterPro; IPR000712; Bcl2 BH.
DR InterPro; IPR003093; Bcl2 BH4.
DR InterPro; IPR002475; BCL2 family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2 FAMILY; 1.
DR PROSITE; PS1080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Alternative splicing; Apoptosis; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 62 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 Potential.
FT VARSPIC 185 229 ERFVLYGNNAELRKQGTENKMLLTGATVAGVLLGSL
FT LSRK -> VRTALP (in isoform Short).
FT FTId=VSP_000514.
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04CCE9DA CRC64;
Query Match 16.7%; Score 184; DB 1; Length 229;
Best Local Similarity 23.9%; Pred. No. 3.9e-08;
Matches 55; Conservative 33; Mismatches 92; Indels 50; Gaps 6;

QY 27 VAQDTEEVFRSYFYRHOQ-----EQEAG-----VAAPADPEMV----- 61
DB 1 MSSNRELVIDFVSKLSQRGHCWSELEEDENRTDTAAEAEMDSVLNGSPSWHPFAGHV 60
QY 62 -----TLPQSSSTMGVGRQALAIIGDINERYDSEFTMLQHLQPTAEAYEYFT 112
DB 61 VNGATVHRSSLEVHIVRASDVQALRDAGDDEFURYRAFSDLTSLQHLITPGTAYQSF 120
QY 113 KIATSLFESGINWGRVALLGFGYRLALHYGHGTGFLGVQTVFVDFMLHHCIAWIA 172
DB 121 QVYNELFHDGVNWRIVAFPSFGGALCVESVDKEMRLVGRIVSWMTYLTIDH-LDPW 179
QY 173 QRGQWV-----AALNLGNP-----ILNLVLVLGVLLGQFVVVR 207
DB 180 ENGGMERFVDLYGNNAELRKQGTENKMLLTGATVAGVLLGSLSRK 229
RESULT 15
BCL2_CHICK STANDARD; PRT; 233 AA.
ID BCL2_CHICK
AC Q00709;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN Name=BCL2; Synonyms=BCL-2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Teijimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell lymphoma;
RX MEDLINE=92379084; PubMed=1511008;
RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncoprotein.";
RL Biochim. Biophys. Acta 1132:109-113(1992).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, thymus. In the embryo, highly levels expressed in all tissues with high levels in the bursa of Fabricius.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
CC -!- SIMILARITY: Belongs to the Bcl-2 family.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; D11382; BAA01978.1; --
DR EMBL; D11381; BAA01978.1; JOINED.
DR EMBL; Z11961; CAA78018.1; --
DR PIR; A37332; A37332.
DR PIR; S24390; S24390.
DR HSP; P10415; IGSM.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR TIGRfams; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 Potential.
FT CONFLICT 64 64 E -> S (in Ref. 2).
FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPLRGCA (in
Ref. 2).
FT CONFLICT 121 121 H -> T (in Ref. 2).
FT CONFLICT 139 139 G -> V (in Ref. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6E4C3D CRC64;

Query Match 16.6%; Score 183.5; DB 1; Length 233;
Best Local Similarity 26.9%; Pred. No. 4.4e-08;
Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

QY 2 ASSGG-PGPRCEGCEPALPSASEEQVAQDTEEVERSVYFVYHQEQEAGVAAAPADPE 59
Db 31 AGEDRPVPP-----APA-PAAPAAVA-----AAGASSHRRPEPPGSAASEVPPA 77
QY 60 MVTLPQPSSTMGQGRQLAI--IGDDINRRYDSEFQTMLOHQAENAYEYFTKIATS 117
Db 78 EGLRPAPP-----GVHLALRQAGDEFSSRYQRDFQMSGQLHLPFTAHGCFVAVVEE 130
QY 118 LPESGINWGRVVALGFGYRLALHYVQHLTGFLQGVTRFVVDFMLHHCIARWIAQRGW 177
Db 131 LFRDGVNWRGRIVAFFEFGGVMCVESYNREMSPLVDNIATMTTEYLNRL-LHNWIQDNGW 189
QY 178 VAALNL-GNG--PI-----INLVVLGVLLG 201
Db 190 DAFVELYGNRMPLDFDFSWISLTKILSLVVG 221

Search completed: December 6, 2004, 16:11:48
Job time : 196 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 16:03:06 ; Search time 38 Seconds
(without alignments)
534.256 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGQGFPPRQCEGPALP.....LVVLGVLLGQFVRRFKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	100.0	211	2 S58873	Bak protein - huma
2	1075	97.5	211	2 S58875	cdn-2 protein - hu
3	189.5	17.2	205	1 TVHUB1	transforming prote
4	189	17.1	239	1 TVHUA1	transforming prote
5	183.5	16.6	233	2 A37332	transforming prote
6	181	16.4	233	2 I49056	bcl-x long - mouse
7	181	16.4	233	2 S51761	BCL-X protein - ra
8	180	16.3	233	2 D47537	apoptosis regulato
9	178.5	16.2	199	1 TVMSB1	transforming prote
10	177	16.0	236	1 TVMSA1	transforming prote
11	176.5	16.0	236	2 I53744	gene bcl-2 protein
12	174.5	15.8	216	2 B77332	transforming prote
13	173.5	15.7	233	2 I67431	transforming prote
14	172.5	15.6	236	2 JC7383	BCL-X-long - rat
15	170.5	15.5	236	2 I67432	BCL-2 - rat (fragm
16	167.5	15.2	190	2 A47537	apoptosis regulato
17	164	14.9	237	2 JE0203	apoptosis regulato
18	160.5	14.6	232	2 S24390	transforming prote
19	158.5	14.4	214	2 I49057	bcl-x transmembran
20	148	13.2	218	2 B47538	bcl-2-associated p
21	143.5	13.0	350	2 A47476	BCL2 homolog Mcl1
22	143	13.0	192	2 D47538	bcl-2-associated p
23	143	13.0	192	2 A47538	bcl-2-associated p
24	142	12.9	179	2 JC7255	Bax-delta protein
25	126	11.4	133	2 I53295	bcl-2-associated p
26	122	11.1	154	2 I58194	gene bcl-2 protein
27	116	10.5	172	2 I49449	hemopoietic-specif
28	112	10.2	175	2 I39055	Bcl-2 related - hu
29	109	9.9	143	2 I38921	bcl-2-associated p

ALIGNMENTS

RESULT 1
S58873
Bak protein - human
N/A: Alternate names: bcl-2 homolog; cdc-1 protein
C: Species: Homo sapiens (man)
G: Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C: Accession: S58873; S58872; S58874
R: Chittenden, I.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.
Nature 374, 733-736, 1995
A: Title: Induction of apoptosis by the Bcl-2 homologous Bak.
A: Reference number: S58873; MUID:95231653; PMID:7715730
A: Accession: S58873
A: Status: preliminary; nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-211 <CHI>
A: Cross-references: UNIPROT:Q16611; EMBL:X84213; NID:G758797; PIDN:AAA93066.1; PID:G758797
R: Farrow, S.N.; White, J.H.M.; Martinou, I.; Raven, T.; Pun, K.T.; Grinham, C.J.; Martini
Nature 374, 731-733, 1995
A: Title: Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.
A: Reference number: S58872; MUID:95231652; PMID:7715729
A: Accession: S58872
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-211 <FAR>
A: Cross-references: EMBL:X84213; NID:G804984; PIDN:CAA58897.1; PID:G804985
R: Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr,
Nature 374, 736-739, 1995
A: Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
A: Reference number: S58874; MUID:95231654; PMID:7715731
A: Accession: S58874
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-211 <KIE>
A: Cross-references: EMBL:U16811; NID:G959523; PIDN:AAA74466.1; PID:G959524
C: Genetics;
A: Gene: GDB:BAK
A: Cross-references: GDB:635887

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.3e-93;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASGQGFPPRQCEGPALPSAEEQVAQTEEVFRSYVYRHHQCEAGVAAAPDEM 60
DB 1 MASGQGFPPRQCEGPALPSAEEQVAQTEEVFRSYVYRHHQCEAGVAAAPDEM 60
QY 61 VTLPQSSSTMGQVGRQLAIIGDDINRRYDSEFTMLQHLQPTAENAYEFTKIATSLFE 120
DB 61 VTLPQSSSTMGQVGRQLAIIGDDINRRYDSEFTMLQHLQPTAENAYEFTKIATSLFE 120
QY 121 SGINWGRVALLGCGYRLALHYVHGLTGFLGQVTRFVDFMLHCHICARVIAORGWVAA 180

NR-13 protein - qu
conserved hypotet
Mcl-1a protein - z
cation transp
cation transp
dnaJ-related prote
band 3-related pro
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
hypothetical prote
odx protein - frui
tenascin-like prot
gop protein - sac
band 3 protein, no

Db 121 SGINRGVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWAA 180
 QY 181 LNLGNGPILNLVGLGVLGQFVVRFPKS 211
 Db 181 LNLGNGPILNLVGLGVLGQFVVRFPKS 211

RESULT 2
 S58875
 cdn-2 protein - human
 C;Species: Homo sapiens (man)
 C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S58875
 R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umanaky, S.R.; Tomei, L.D.; Barr, Nature 374, 736-739, 1995
 A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.
 A;Reference number: S58874; MUID:95231654; PMID:7715731
 A;Accession: S58875
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-211 <KIE>
 A;Cross-references: UNIPROT:Q13014; EMBL:U16812; NID:G595925; PIDN:AAA74467.1; PID:G5959
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

Query Match 97.5%; Score 1075; DB 2; Length 211;
 Best Local Similarity 97.2%; Pred. No. 2.9e-90;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGQGPGRPECGPAPLPSASEQVADTEVFRSYVYFHQOEQAEGVAPADPEM 60
 Db 1 MASGQGPGRPECGPAPLPSASEQVADTEVFRSYVYFHQOEQAEGVAPADPEM 60

QY 61 VTLPQPSSTMGVQGLAIIGDDINRRYDSFQMLQHLQPTAENAYEYFTKIATSLFE 120
 Db 61 VTLPQPSSTMGVQGLAIIGDDINRRYDSFQMLQHLQPTAENAYEYFTKIATSLFE 120

QY 121 SGINRGVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWAA 180
 Db 121 SGINRGVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIARWIAQRGGWAA 180

QY 181 LNLGNGPILNLVGLGVLGQFVVRFPKS 211
 Db 181 LNLGNGPILNLVGLGVLGQFVVRFPKS 211

RESULT 3
 TVHUB1
 transforming protein bcl-2, splice form beta - human
 N;Alternate names: apoptosis regulator bcl-2
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C;Accession: B29409; I52566; D37332
 R;Tsujimoto, Y.; Croce, C.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A;Reference number: A29409; MUID:86259760; PMID:3523487
 A;Accession: B29409
 A;Molecule type: mRNA
 A;Residues: 1-205 <TSU>
 A;Cross-references: UNIPROT:P10415; GB:M13995; NID:G179368; PIDN:AAA51814.1; PID:G179369
 R;Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.
 Blood 79, 229-237, 1992
 A;Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H
 A;Reference number: I52566; MUID:92096610; PMID:1339299
 A;Accession: I52566
 A;Status: translated
 A;Molecule type: DNA
 A;Residues: 1-131 <TAN>
 A;Cross-references: GB:S72602; NID:G241046; PIDN:AADI4111.1; PID:G4261811
 R;Tsujimoto, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
 A;Reference number: A37332; MUID:92375724; PMID:1508712

A;Accession: D37332
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: DNA
 A;Residues: 1-33,'E',34-95,'T',97-109,'R',111-205 <EGU>
 C;Genetics:
 A;Gene: GDB:BCL2
 A;Cross-references: GDB:119031; OMIM:151430
 A;Map position: 18q21.3-18q21.3
 C;Function:
 A;Description: blocks apoptosis in hematopoietic cells
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 17.2%; Score 189.5; DB 1; Length 205;
 Best Local Similarity 27.4%; Pred. No. 8.1e-10;
 Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;

QY 30 DTEVFRSYVYFHQO---EQEAGV-----AAPA-----DPEWVT 62
 Db 10 DNEIVMKYIHYKLSQRYEWDAGDYGAAPGAPGAFSSQPGHTPHPAASRDVPART 69

QY 63 LPLO-PSSTMGQVGRQIAI-----GDDINRRYDSFQMLQHLQPTAENAYEY 110
 Db 70 SPLQTPAAPGAAAGPALSPVPPVHVALRQAGDFFSRVYRGDFAEISSQLHTPTARGR 129

QY 111 FTKIATSLFESGINRGVALLGFGYRLALHYQHGLTGLGQVTRFVVDFMLHHCIAEW 170
 Db 130 FATVVEELFRDGVNMGVIVAFEFEGVCMCVSVNREMSPLVDNIALMWTLYLNRH-LHTW 188

QY 171 IAORGWVAA---LNLG 184
 Db 189 IODNGGWGASGDVSLG 205

RESULT 4
 TVHUB1
 transforming protein bcl-2, splice form alpha - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
 A;Reference number: A37332; MUID:92375724; PMID:1508712
 A;Accession: C37332
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-239 <EGU>
 A;Cross-references: UNIPROT:P10415
 A;Note: this report is a correction
 R;Tsujimoto, Y.; Croce, C.W.
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
 A;Reference number: A29409; MUID:86259760; PMID:3523487
 A;Accession: A29409
 A;Molecule type: mRNA
 A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
 A;Cross-references: GB:M13994; NID:G179366; PIDN:AAA51813.1; PID:G179367
 A;Note: this sequence has been corrected in reference A37332
 R;Sto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldmann, P.; Korsmeyer
 EMBO J. 7, 123-131, 1988
 A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
 A;Reference number: S02452; MUID:88196071; PMID:2834197
 A;Accession: S02452
 A;Molecule type: mRNA
 A;Residues: 1-239 <SET>
 R;Cleary, M.L.; Smith, S.D.; Sklar, J.
 Cell 47, 19-28, 1986
 A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglob
 A;Reference number: A24428; MUID:87002488; PMID:2875799
 A;Accession: A24428
 A;Molecule type: mRNA
 A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>

A:Cross-references: GB:MI4745; NID:gl79370; PIDN:AAA35591.1; PID:gl79371
R:Riha, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
OncoGene Res. 2, 263-275, 1988
A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
A:Reference number: A27622; MUID:88217344; PMID:3285301
A:Accession: A27622
A:Molecule type: mRNA
A:Residues: 1-58, 'T', 60-239 <HUA>
A:Accession: B27622
A:Molecule type: DNA
A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA>
A:Note: the sequence was determined from the germline gene
C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
C:Genetics:
A:Gene: BCL2
A:Cross-references: GDB:119031; OMIM:151430
A:Map position: 18q21.3-18q21.3
C:Function:
A:Description: blocks apoptosis in hematopoietic cells
C:Superfamily: bcl apoptosis regulator, inhibitory type
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto:
Query Match 17.1%; Score 189; DB 1; Length 239;
Best Local Similarity 26.4%; Pred. No. 1 le-09;
Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;
30 DTEVFRSYVYRHQ---EQEAGV-----AAPA-----DPEVMT 62
10 DNRBIVNKYIHYKLSRGVWDAGDYCAAPGAPAFGIFSSQPGHTPHPAASRDVPART 69
63 LPLO-PSSTWQGVCRQLAII-----GDDINRVDSEFQTMQLHQJTAENAVEY 110
70 SFLQTPAAGAAAGALPSPVPPVVVHLTLRQAGDDFSRRYRDFFAEMSKLHTPTFARGR 129
111 FTKIATSLFESGINWGRVVALLGFGYRLAHVYQHLTGLGQVTRFVDFVDFMLHRCIARW 170
130 FATVVEELFRDGVNNGRIVAFEFEGGVNVCVESVNRMSPLVDNIALWTEYLNRH-LHTW 188
171 IAQRGGVVAALNLGNPGI-----LNLVVLGVVLGG 201
189 IQDNGGWDAFVEL-YGFSMRFLDFFSWLSKLTLLSLALVG 227
RESULT 5
A37332
transforming protein (bcl-2-alpha) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A37332; S35453
R:Equchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A:Reference number: A37332; MUID:92375724; PMID:1508712

Query Match 16.6%; Score 183.5; DB 2; Length 233;
Best Local Similarity 26.9%; Pred. No. 3.4e-09;
Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

2 ASGGG--PGPPRCGCEPALPSASEQVADTEEVFRSVYFVRHOQECAEGVAAPADPE 59
| | | | | | | | | | | | | | | | | | | | | |
31 AAGEDREVPFP-----APA-PAAAPAAVA-----AAGASSHHRRPFGGSAASEVPPA 77
| | | | | | | | | | | | | | | | | | | | | |

60 MVTLPLQSPSTMCGVGRQLAI--IGDDINRYDSEFTMLQLHQTAEANVEYETKIATS 117
| | | | | | | | | | | | | | | | | | | | | |

Status: nucleic acid sequence not shown
Molecule type: DNA
Residues: 1-233 <ECU>
Cross-references: UNIPROT:Q00709; EMBL:D11381
Genetics:
Introns: 189/3
Superfamily: bcl apoptosis regulator, inhibitory type
Keywords: mitochondrion; transforming protein; transmembrane protein

```

Dc 78 EGLRPAPP-----GVHLALRQAGDEFRSRRYQRDFQAQMSGQLHLTPPTAFHGRFVAVVEE 130
Qy 118 LFESGINNGRVALLGFGYRLAHVYQHLGFLGFGQVTRFVVDFMLHHCIARWIAQRGSW 177
Db 131 LFRGVNNGRIVAFEFEGGVNVCVSIVREMSPLVDNIATWNTYLNRRH-LHNWIQDNGGW 189
Qy 178 VAALNL-GNG--PI-----LNLVVLGVLLG 201
Db 190 DAFVELYGNMRPLDFDSWISLKITLSLVLG 221

RESULT 6
bcl-x long - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49056; S52866
E:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
A:Reference number: I49055; MUID:95052604; PMID:7963517
A:Accession: I49056
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: UNIPROT:Q64373; EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G506647
R:Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A:Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thro
A:Reference number: S52866
A:Accession: S52866
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-233 <KAM>
A:Cross-references: EMBL:X83574; NID:g965622; PIDN:CAA58557.1; PID:g965623
C:Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 16.4%; Score 181; DB 2; Length 233;
Best Local Similarity 28.3%; Pred. No. 5.7e-09;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

Qy 71 MGQVGROLAIGDDINRRYDSEFTMLQHLQPTAENAYEFTKIATSI.FESSIGNKRVVA 130
Db 83 MAAVKQALRAGDEFEELRYRAFSDLTLSQLHTPGTAYQSFQEVQNEUFRDGVNNGRIVA 142
Qy 131 LLGFGYRLAHVYQHLGFLGQVTRFVVDFMLHHCIARWIAQRGSWVAALNL-GNGP-- 187
Db 143 FFEFGGALCVESVDKXNQVLVSRIASWNTYLNDRH-LEPWIQENGGWDTFVDLYGNAAA 201
Qy 188 -----LNLVVLGVLLGQFVRR 207
Db 202 ESRKGQERFNRFELTGMTVAGVLLGSLFSRK 233

```

RESULT 7
S51761
BCL-X protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S51761; S51762
R/Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A/Reference number: S51761
A/Accession: S51761
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-233 <MIC>
A/Cross-references: UNIPROT:P53563; EMBL:X82537; NID:5607176; PID:CAA57886.1; PID:9607
A/Experimental source: embryonic; brain
A/Status: S51762
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 189-233 <WT>

A;Cross-references: EMBL:X82537; NID:G607176; PIDN:CAA57887.1; PID:G607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics: 125/3
A;Introns: 125/3
C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 16.4%; Score 181; DB 2; Length 233;
Best Local Similarity 28.3%; Pred. No. 5.7e-09;
Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;

QY 71 MGQVGRQLAIGDINRRYDSFQMLQLOPTANAYEYFKIATSLFESGINGRVVA 130
DB 83 MAAVKQALREAGDEFELRYRAFSDLTSLHTPTAYQSFQVNVNELFRDGVNNGRIVA 142
QY 131 LLGFGYRLALHYVQHGLTGLGQVTRFVVDVFLMHLHCIARWIAQRCGWAAALNL-GNGP-- 187
DB 143 FFSFGGALCVESVDKEMQVLVSRASWATYLNDR-LRPWQENGWDTFVDLYGNNA 201
QY 188 -----ILNVLVVLGVVLLGQFVVR 207
DB 202 ESRKQGRFNRWFLTGMTVAGVLLGLSLFRK 233

RESULT 8

B47537
A;Title: apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein
A;Contains: apoptosis regulator bcl-xS
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977; PMID:8358789
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-233 <BO1>
A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:G510900; PIDN:CAA80661.1; PID:G510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>
A;Cross-references: GB:L20122; NID:G623236; PIDN:CAA80662.1; PID:G623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <A2>

Query Match 16.4%; Score 180; DB 2; Length 233;
Best Local Similarity 28.3%; Pred. No. 7e-09;
Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;

QY 71 MGQVGRQLAIGDINRRYDSFQMLQLOPTANAYEYFKIATSLFESGINGRVVA 130
DB 83 MAAVKQALREAGDEFELRYRAFSDLTSLHTPTAYQSFQVNVNELFRDGVNNGRIVA 142
QY 131 LLGFGYRLALHYVQHGLTGLGQVTRFVVDVFLMHLHCIARWIAQRCGWAAALNL-GNGP-- 187
DB 143 FFSFGGALCVESVDKEMQVLVSRASWATYLNDR-LRPWQENGWDTFVDLYGNNA 201

QY 188 -----ILNVLVVLGVVLLGQFVVR 207
DB 202 ESRKQGRFNRWFLTGMTVAGVLLGLSLFRK 233

RESULT 9

TWMSB1

transforming protein bcl-2-beta - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: B25960
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A;Reference number: A90893; MUID:87187643; PMID:3032455
A;Accession: B25960
A;Molecule type: DNA
A;Residues: 1-199 <NEG>
A;Cross-references: UNIPROT:P10417; GB:M16506; NID:G468335; PIDN:AAA37281.1; PID:G387110
C;Genetics:
A;Gene: BCL2
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; transforming protein

Query Match 16.2%; Score 178.5; DB 1; Length 199;
Best Local Similarity 25.1%; Pred. No. 7.8e-09;
Matches 49; Conservative 25; Mismatches 84; Indels 37; Gaps 5;

QY 22 ASBEQVAQDTEEVRSYVFRHQE-----QEAEGVAAP--ADPEMTLPQP-SSTMGOV 74
DB 2 AQAGRTGYDNRREIVMKYIHYKLSQRYEWDAADAAAPLGAAPTGGIFSFQPSNPMPAV 61

QY 75 GRQLAI-----IGDINRRYDSEFQTMQLQHPQTA 105
DB 62 HREMAARTSLRLVATAGPALSPPVPCVHLTRRAGDFFSRYYRDRFAEMSSQLHLTF 121

QY 106 NAYEYFTKIATSLFESGINGRVVALGFGYRLALHYVQHGLTGLGQVTRFVVDVFLMHL 165
DB 122 TARGFATVVEELFRDGVNNGRIVAFEFGGVCMVESVNRMSPLVDNIALMWTYINRH 181

QY 166 CIAEWTAQRGGWAA 180
DB 182 -LHTWIDQNGWVGA 195

RESULT 10

transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A;Reference number: A90893; MUID:87187643; PMID:3032455
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:G468336; PIDN:AAA37282.1; PID:G387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res 20, 4187-4192, 1992

A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>
C;Genetics:
A;Gene: BCL2

A;Introns: 192/3
C;Superfamily: bcl apoptosis regulator, inhibitory type
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane protein

Query Match 16.0%; Score 177; DB 1; Length 236;
Best Local Similarity 25.1%; Pred. No. 1.3e-08;
Matches 52; Conservative 27; Mismatches 90; Indels 38; Gaps 6;

QY 22 ASBEQVAQDTEEVRSYVFRHQE-----QEAEGVAAP--ADPEMTLPQP-SSTMGOV 74
DB 2 AQAGRTGYDNRREIVMKYIHYKLSQRYEWDAADAAAPLGAAPTGGIFSFQPSNPMPAV 61

```
QY 75 GRQLAI-----IGDDINRRYDSFQTMQLHQPTAE 105
Db 62 HREMAARTSPRLPLVATAGPALSPVPPCVHLTLRRAGDFFSRYYRRDRFAEMSSQLHLTPF 121
QY 106 NAYEYFTKIATSLFESGINRGVVALLGFGYRLALHVVYQHGLTGLGQVTRFVVDFMLHH 165
Db 122 TARGRFATVVELFRDGVNMGRIVAFPEFGVCMCVSNREMSPLVDNIALMWTETYLNRH 181
QY 166 CIARWIAQRGGWVAALNLGNPILNVL 192
Db 182 -LHTWIQDNGGDFAVEL-YGPSMRPL 206

RESULT 11
153744
Gene bcl-2 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I53744
R/Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A/Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A/Reference number: I53744; MUID:94193015; PMID:8144041
A/Accession: I53744
A/Molecule type: mRNA
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-236 <RES>
A/Cross-references: UNIPROT:P49950; GB:L14680; NID:9408946; PIDN:AAAS3662.1; PID:g408947
C/Genetics:
A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 16.0%; Score 176.5; DB 2; Length 236;
Best Local Similarity 24.2%; Pred. No. 1.5e-08;
Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 ASEQVAQDTEVFRSVFYRHQ-----EQEAGVAAPA----- 56
Db 2 AQAGRTGYDNKEIMVKYIHKLSQGVYEWDTGDSAPLRAAFTPGIFSQPSNRTPAV 61
QY 57 --DPENVTLPLQSSSTMGVGRQLAI-----GDDINRRYDSFQTMQLHQPT 103
Db 62 HRDTAARTSPRLP--LVANAGPALSPVPVHVHLTLRRAGDFFSRYYRRDRFAEMSSQLHLT 119
QY 104 AENAYEYFTKIATSLFESGINRGVVALLGFGYRLALHVVYQHGLTGLGQVTRFVVDFML 163
Db 120 PFTARGRFATVVELFRDGVNMGRIVAFPEFGVCMCVSNREMSPLVDNIALMWTETYLNRH 179
QY 164 HHCIARWIAQRGGWVAALNLGNPFI-----LNVLVVLGVVLG 201
Db 180 RH-LHTWIQDNGGDFAVEL-YGPSMRPLPFDLSWLSKTLISLALVG 224

RESULT 12
B37332
Transforming protein (bcl-2-beta) - chicken
C/Species: Gallus gallus (chicken)
C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
C/Accession: B37332; S35452
R/Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A/Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues.
A/Reference number: A37332; MUID:92375724; PMID:1508712
A/Accession: B37332
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-216 <EGU>
A/Cross-references: EMBL:D11381; EMBL:D11382
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.8%; Score 174.5; DB 2; Length 216;
Best Local Similarity 27.3%; Pred. No. 2e-08;
```

```
Matches 50; Conservative 27; Mismatches 81; Indels 25; Gaps 7;
QY 2 ASGQG--PGPPRQCEGEPALPSAEEQVAQDTEEVFRSVFYRHQEQEAEAGVAAPADPE 59
Db 31 AAGEDEPPVPP-----APA-PAAPAAVA-----AAGASSHHRPEPPGSAASEVPPA 77
QY 60 MVTLPQSSSTMGVGRQLAI--IGDDINRRYDSFQTMQLHQPTAENAYEYFTKIATS 117
Db 78 EGLRPAPP-----GVHLAFQAGDEFSRRYQRDFAQMSGQLHLTPPTAHGRFVAVVEE 130
QY 118 LFESGINRGVVALLGFGYRLALHVVYQHGLTGLGQVTRFVVDFMLHHCIAEWIAQRGGW 177
Db 131 LFRDGVNMGRIVAFPEFGVCMCVSNREMSPLVDNIALMWTETYLNRH-LHNWIQDNGGW 189
QY 178 VAA 180
Db 190 VEA 192

RESULT 13
167431
BCL-X-Long - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I67431
R/Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A/Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A/Reference number: I53295; MUID:95129487; PMID:7828536
A/Accession: I67431
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-233 <RES>
A/Cross-references: UNIPROT:P53563; EMBL:U34963; NID:G1004376; PIDN:AAA7686.1; PID:g1010
C/Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.7%; Score 173.5; DB 2; Length 233;
Best Local Similarity 27.6%; Pred. No. 2.7e-08;
Matches 48; Conservative 25; Mismatches 78; Indels 23; Gaps 5;

QY 49 AEGVAAPADPEMVTLPQSSSTMGVGRQLAIIGDDINRRYDSFQTMQLHQPTAENAY 108
Db 68 ATGHSSLDAREV-LP-----MAAVKQALREAGDEFELRYRAFSDLTSLQHLTPGVTV 120
QY 109 EYFTKIATSLFESGINRGVVALLGFGYRLALHVVYQHGLTGLGQVTRFVVDFMLHHCIA 168
Db 121 QSFQVVELFRDGVNMGRIVAFSSFGALCVESVDKEMQVLSRIASWMTATYLNLDH-LE 179
QY 169 RWIAQRGGWVAALNL-GNGP-----ILNVLVVLGVVLGQFVVR 207
Db 180 PWIQENGWDFTVDLYGNNTAPESRKGQERNRWFLLTGMTVAGVVLGSLFSRK 233
```

```
RESULT 14
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C/Species: Cricetulus griseus (Chinese hamster)
C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C/Accession: JC7383
R/Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A/Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A/Reference number: JC7383
A/Contents: Ovary
A/Accession: JC7383
A/Molecule type: mRNA
A/Residues: 1-236 <TON>
A/Cross-references: UNIPROT:Q9JUV8; GB:A0271720
C/Comment: This protein has anti-apoptotic function, and supports cell survival.
C/Genetics:
A/Gene: bcl-2
C/Superfamily: bcl apoptosis regulator, inhibitory type
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us-09-633-200-7.rpr

Mon Dec 6 16:29:28 2004

C;Keywords: B-cell lymphoma; ovary

Query Match 15.6%; Score 172.5; DB 2; Length 236;
 Best Local Similarity 24.4%; Pred. No. 3.4e-08;
 Matches 55; Conservative 30; Mismatches 93; Indels 47; Gaps 7;

QY 22 ASEEQVAQDTEEVFRSYVYRHOEQ-----EAGVAAPA- 56
 DB 2 AQAGRTGYDNREIVMKYIHKLSQGYEWVDGVDAAALGAAPTGIFSFQPSNRTPAV 61

QY 57 --DPENVTLPLQF--SSTMQ-----VGRQLAIGDDINRRYDSHFQTMLOHLOPTAE 105
 DB 62 HRDMAARTSPLRPVATTGPTLSPVPVHLTLRRAGDDFSRRYRDDFAEMSSQLHLTPF 121

QY 106 NAYEYFTKIATSLFESGINWGRVALLGFGYRLAHVYQHGLTGFLGQVTRFVVDFMLHH 165
 DB 122 TARGREFAIVVEELFRDGVNWRIVAFEFEGGVNVCESVNRNEMPLVDNIALMWTBYLN 181

QY 166 CIARWIAQRGWVAALNLGNP-----LNVLVILGVVLLG 201
 DB 182 -LHTWIQDNGWDFAVEL-YGFSVRELFDFSNLSKLTLLSLALVG 224

RESULT 15
 I67432
 BCU-2 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I67432
 R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equivalent constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.
 A;Reference number: I53295; MUID:95129487; PMID:7828536
 A;Accession: I67432
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-236 <RES>
 A;Cross-references: UNIPROT:P49950; EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004378
 C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match 15.5%; Score 170.5; DB 2; Length 236;
 Best Local Similarity 23.3%; Pred. No. 5.2e-08;
 Matches 53; Conservative 30; Mismatches 93; Indels 51; Gaps 7;

QY 22 ASEEQVAQDTEEVFRSYVYRHOEQ-----EAGVAAPA- 56
 DB 2 AQAGRTGYDNREIVMKYIHKLSQGYEWDTGDSAPLRRAPTGIFSFQPSNRTPAV 61

QY 57 --DPENVTLPLQSSTMQVGRQLAI-----GDDINRRYDSHFQTMLOHLOPT 103
 DB 62 HRDTAARTSPLRP--LVANAGPALSPVPVPHLTLRRAGDDFSRRYRDDFAEMSSQLHLT 119

QY 104 AENAYEFTKIATSLFESGINWGRVALLGFGYRLAHVYQHGLTGFLGQVTRFVVDFML 163
 DB 120 PFTARGREFAIVVEELFRDGVNWRIVAFEFEGGVNVCESVNRNEMPLVDNIALMWTBYLN 179

QY 164 HHCIARWIAQRGWVAALNLGNPILNVL-----VVLGVVILG 201
 DB 180 RH-LHTWIQDNGWDFAVEL-YGFSMRPLDFDSWQSLKLTLLSLALVG 224

Search completed: December 6, 2004, 16:12:32
 Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: December 6, 2004, 16:11:57 ; Search time 141 Seconds
(without alignments)
533.670 Million cell updates/sec

Title: US-09-633-200-7
Perfect score: 1103
Sequence: 1 MASGQGFPPRCQCBPALP.....LVVLGVLLGQFVRRFFKS 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	100.0	211	14	US-10-101-482-7
2	1103	100.0	211	14	US-10-101-482-10
3	1103	100.0	211	14	US-10-189-294-2
4	1103	100.0	211	14	US-10-177-293-25
5	1103	100.0	211	15	US-10-003-632C-6
6	1103	100.0	211	17	US-10-825-282-34
7	1088.5	98.7	210	14	US-10-101-482-22
8	1075	97.5	211	14	US-10-101-482-9
9	1075	97.5	211	14	US-10-101-482-11
10	625	56.7	117	14	US-10-189-294-4
11	609	55.2	116	14	US-10-189-294-5
12	236	21.4	45	9	US-09-971-980-39
13	214.5	19.4	99	15	US-10-294-445-26

14	192	17.4	205	13	US-10-087-192-1956	Sequence 1956, Appl
15	192	17.4	239	15	US-10-148-953A-4	Sequence 4, Appli
16	191	17.3	239	15	US-10-287-321-2	Sequence 2, Appli
17	190	17.2	239	8	US-08-726-211-5	Sequence 5, Appli
18	190	17.2	239	10	US-09-993-420A-8	Sequence 8, Appli
19	190	17.2	239	14	US-10-101-482-12	Sequence 12, Appli
20	190	17.2	239	14	US-10-072-830-2	Sequence 2, Appli
21	190	17.2	239	14	US-10-141-618-12	Sequence 12, Appli
22	190	17.2	239	14	US-10-053-645A-21	Sequence 21, Appli
23	190	17.2	239	14	US-10-387-961A-5	Sequence 5, Appli
24	190	17.2	239	15	US-10-003-632C-1	Sequence 1, Appli
25	190	17.2	239	15	US-10-003-632C-3	Sequence 3, Appli
26	190	17.2	239	15	US-10-148-953A-1	Sequence 1, Appli
27	190	17.2	239	15	US-10-148-953A-3	Sequence 3, Appli
28	190	17.2	239	16	US-10-450-366-4	Sequence 4, Appli
29	190	17.2	239	17	US-10-770-568-16	Sequence 16, Appli
30	190	17.2	239	17	US-10-825-282-46	Sequence 46, Appli
31	189.5	17.2	205	8	US-08-726-211-7	Sequence 7, Appli
32	189.5	17.2	205	9	US-09-952-278-4	Sequence 4, Appli
33	189.5	17.2	205	14	US-10-053-645A-23	Sequence 23, Appli
34	189.5	17.2	205	14	US-10-387-961A-7	Sequence 7, Appli
35	189.5	17.2	205	15	US-10-003-632C-2	Sequence 2, Appli
36	189.5	17.2	205	15	US-10-003-632C-11	Sequence 11, Appli
37	189	17.1	239	14	US-10-277-693A-10	Sequence 10, Appli
38	189	17.1	239	15	US-10-003-632C-10	Sequence 10, Appli
39	189	17.1	239	15	US-10-003-632C-13	Sequence 13, Appli
40	189	17.1	239	15	US-10-148-953A-2	Sequence 2, Appli
41	189	17.1	239	15	US-10-148-953A-5	Sequence 5, Appli
42	184	16.7	229	16	US-10-659-705-7	Sequence 7, Appli
43	183	16.6	36	11	US-09-828-870-14	Sequence 14, Appli
44	183	16.6	179	14	US-10-402-017-6	Sequence 6, Appli
45	182	16.5	199	14	US-10-402-017-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-101-482-7
Sequence 7, Application US/10101482
Publication No. US2003000837A1
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10101482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792

```
;
;
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-101-482-7

Query Match      100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGQGPPECEGCEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
DB 1 MASGGQGPPECEGCEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFMHLHICIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFMHLHICIARWIAQRGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211

RESULT 2
US-10-101-482-10
; Sequence 10, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORESTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
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; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-101-482-10

Query Match      100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGQGPPECEGCEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
DB 1 MASGGQGPPECEGCEPALPSASEEQVAQDTEEVRSYVYVRHQEQEAGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFMHLHICIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVFMHLHICIARWIAQRGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRPFKS 211

RESULT 3
US-10-189-294-2
; Sequence 2, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; GIBSON, HELEN L.
; FITZPATRICK, PAUL A.
; BARR, PHILIP J.
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA
; ENCODING THE PROTEIN, AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-189-294-2

Query Match      100.0%; Score 1103; DB 14; Length 211;
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Best Local Similarity 100.08; Pred. No. 8.6e-101;					
Matches	211;	Conservative	0;	Mismatches	0;
				Indels	0;
Gaps	0;				
Qy	1	MASGGGPPPRQCEGPALPSASBEQVAQDTEEVFRSYVYRHHQQEQEAGVAAADPEM	60		
Dd	1	MASGGGPPPRQCEGPALPSASBEQVAQDTEEVFRSYVYRHHQQEQEAGVAAADPEM	60		
Qy	61	VTLPLQPSTMGQVRQLAIGDDINRRYDSEFOTLQHLQPTAEANAYEFFKIATSLFE	120		
Dd	61	VTLPLQPSTMGQVRQLAIGDDINRRYDSEFOTLQHLQPTAEANAYEFFKIATSLFE	120		
Qy	121	SGINGRVVALLGFGYRLAHVGHGTGLQGVTFRVDFMLHHCIAWIAQRGWAA	180		
Dd	121	SGINGRVVALLGFGYRLAHVGHGTGLQGVTFRVDFMLHHCIAWIAQRGWAA	180		
Qy	181	LNLNGPILNVLWLGVLLQGFVRRFFKS	211		
Dd	181	LNLNGPILNVLWLGVLLQGFVRRFFKS	211		

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RESULT 4
US-10-177-293-25
; Sequence 25, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kanatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-25

Query Match 100.0%; Score 1103; DB 14; Length 211;
Best Local Similarity 100.0%; Pred.No. 8.6e-101; Indels 0; Gaps 0;
Matches 211; Conservative 0; Mismatches 0;

QY 1 MASGGGPGPRCEGCEPALFSASEEQVADTTEVFRSYVFRHQOEAEQVAAAPDEM 60

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RESULT 5
US-10-003-632C-6
; Sequence 6, Application US/10003632C
; Publication No. US20040043028A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei
; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or
; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei
; FILE REFERENCE: CEN0269
; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-6

Query Match      100.0%; Score 1103; DB 15; Length 211;
Best Local Similarity 100.0%; Pred. No. 8,6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MASGQGGPPRQCGGEPALPSASAEQVAQDTEEVFRSYVYRHHQOEAEAGVAAPADPEM 60
Db      1  MASGQGGPPRQCGGEPALPSASAEQVAQDTEEVFRSYVYRHHQOEAEAGVAAPADPEM 60

Qy      61  VTLPLOPSSSTMGGVGRQLAIIIGDDINRRYDSEFCQTLQHLQPTAENAYEYFTKIATSLFE 120
Db      61  VTLPLOPSSTMGGVGRQLAIIIGDDINRRYDSEFCQTLQHLQPTAENAYEYFTKIATSLFE 120

Qy      121  SGINWGRVVALLGFGYRLALHVYOHGLTGFLGQVTRFVDFMLHHCICARWIAQRGGWAA 180
Db      121  SGINWGRVVALLGFGYRLALHVYOHGLTGFLGQVTRFVDFMLHHCICARWIAQRGGWAA 180

Qy      181  LNLNGGPILNLVVLGVVLIGQFVVRFFKS 211
Db      181  LNLNGGPILNLVVLGVVLIGQFVVRFFKS 211

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RESULT 6
US-10-825-282-34
; Sequence 34, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; METHOD OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29

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; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-04-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 211
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-825-282-34

Query Match      100.0%; Score 1103; DB 17; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.6e-101;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGQGGPPRECCEGEPALPSASEEQVAODTEEVRSYVYVRHQOEQAEGVAAPADPEM 60
DB 1 MASGQGGPPRECCEGEPALPSASEEQVAODTEEVRSYVYVRHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSEFQTMQLHQPDAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSEFQTMQLHQPDAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211

RESULT 7
US-10-101-482-22
; Sequence 22, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-10-101-482-9

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
; US-10-101-482-22

Query Match      98.7%; Score 1088.5; DB 14; Length 210;
Best Local Similarity 99.5%; Pred. No. 2.3e-99;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MASGQGGPPRECCEGEPALPSASEEQVAODTEEVRSYVYVRHQOEQAEGVAAPADPEM 60
DB 1 MASGQGGPPRECCEGEPALPSASEEQVAODTEEVRSYVYVRHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSEFQTMQLHQPDAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMTGQVGRQLAIIGDDINRRYDSEFQTMQLHQPDAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYQHGLTGFLGQVTRFVVDMLHHCIARWIAORGGWVAA 180
QY 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNPILNLVVLGVLLGQFVVRFFKS 211

RESULT 8
US-10-101-482-9
; Sequence 9, Application US/10101482
; Publication No. US20030008837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; BARR, PHILIP J.
; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
; ENCODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
; US-10-101-482-9
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Query Match          97.5%; Score 1075; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 5.1e-98;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0

QY      1 MASGGGPGPPRQCEGPALPSASBEQVAQDTEEVFSVYFRHQOQEAEGVAAAPADPEM 60
DB      1 MASGGGPGPPRQCEGPALPSASBEQVAQDTEEVFSVYFRHQOQEAEGVAAAPADPEM 60

QY     61 VTLPQPSTMGQVGQRQLAI:GDGINRRYSEFOTMLQHLQPTAENAYSYFTKIATSLFE 120
DB     61 VTLPQPSTMGQVGQRQLAI:GDGINRRYSEFOTMLQHLQPTAENAYSYFTKIATSLFE 120

QY    121 SGINGRVVALLGFCGYRLALHYVGHGTGLGQVTRWVDFMLHHCIARWIAQRGGWAAA 180
DB    121 SGINGRVVALLGFCGYRLALHYVGHGTGLGQVTRWVDFMLHHCIARWIAQRGGWAAA 180

QY    181 LNLNGPILNVLVLGVLLGQFVVRFFKS 211
DB    181 LNLNGPILNVLVLGVLLGQFVVRFFKS 211

RESULT 9
US-10-101-482-11
; Sequence 11, Application US/10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL C.
; TITLE OF INVENTION: NOVEL APPOPTOSIS-MODULATING PROTEINS, DNA
; CODING THE PROTEINS AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/101,482
; FILING DATE: 18-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,157
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-101-482-11

Query Match          97.5%; Score 1075; DB 14; Length 211;
Best Local Similarity 97.2%; Pred. No. 5.1e-98;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0

QY      1 MASGGGPGPPRQCEGPALPSASBEQVAQDTEEVFSVYFRHQOQEAEGVAAAPADPEM 60

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QY 131 LLGFGYRLALHYVQGLTGFLGQVTFVVDVFLHHCIARWIAQRGWVAALNLGNP 187
Db 61 LLGFGYRLALHYVQGLTGFLGQVTFVVDVFLHHCIARWIAQRGWVAALNLGNP 117

RESULT 11
US-10-189-294-5
; Sequence 5, Application US/10189294
; Publication No. US20030060615A1
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; Gibson, Helen L.
; Fitzpatrick, Paul A.
; Barr, Philip J.
; TITLE OF INVENTION: A NOVEL BAK BINDING PROTEIN, DNA
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, THERESA A.
; STREET: 1560 Broadway, Suite 1200
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/189,294
; APPLICATION NUMBER: US/10/189,294
; FILING DATE: 01-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/381,488
; FILING DATE: 11-Feb-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, THERESA A.
; REGISTRATION NUMBER: 32,547
; REFERENCE/DOCKET NUMBER: 4147-15-PUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO. 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..116
; OTHER INFORMATION: /note= "Bak (delta)3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-189-294-5
Query Match 55.2%; Score 609; DB 14; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.2e-52;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 MLQHLQPTAENAYEYFKIATSLFESGINWGRVALLGFGYRLALHYVQGLTGFLGQV 155
Db 1 MLQHLQPTAENAYEYFKIATSLFESGINWGRVALLGFGYRLALHYVQGLTGFLGQV 60
QY 156 RFVVDVFLHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQVVRFFKS 211
Db 61 RFVVDVFLHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQVVRFFKS 116

RESULT 12
US-09-971-980-39
; Sequence 39, Application US/09971980
; Patent No. US20020164349A1

GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flavivirus
; TITLE OF INVENTION: Pestiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1e1 Sequence
US-09-971-980-39
Query Match 21.4%; Score 236; DB 9; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 163 LHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQVVR 207
Db 1 LHHCIARWIAQRGWVAALNLGNPILNLVVLGVLLGQVVR 45

RESULT 13
US-10-294-445-26
; Sequence 26, Application US/10294445
; Publication No. US20040023866A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: BACTERIAL BCL-2 DOMAIN-CONTAINING
; TITLE OF INVENTION: POLYPEPTIDES, ENCODING NUCLEIC ACID MOLECULES, AND RELATED
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: P-LJ 5489
; CURRENT APPLICATION NUMBER: US/10/294,445
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/332,964
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-294-445-26
Query Match 19.4%; Score 214.5; DB 15; Length 99;
Best Local Similarity 41.7%; Pred. No. 3e-13;
Matches 40; Conservative 19; Mismatches 36; Indels 1; Gaps 1;
QY 82 GDDINRYDSEFOTMLQHLQPTAENAYEYFKIATSLFESGINWGRVALLGFGYRLALH 141
Db 5 GDELEKXYERVFSSMAVQLHITETARELFTQAGLFSGGINWGRVALLGFGGALAKK 64
QY 142 YIQHGLTGFLGQVTFVVDVFLHHCIARWIAQRGW 177
Db 65 LVNSAMEGLVSRLLADWVVEFLKHN-LAETIQONGW 99

RESULT 14
US-10-087-192-1956
; Sequence 1956, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.

```
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1956
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1956
```

```
Query Match 17.4%; Score 192; DB 13; Length 205;
Best Local Similarity 27.7%; Pred. No. 1.4e-10;
Matches 53; Conservative 25; Mismatches 73; Indels 40; Gaps 6;

QY 30 DTEVFRSYVYRHHQ---EQEAEGV-----AAPA-----DPEMVT 62
DB 10 DNRDIVMKYIHYKLSQRYEWDAGDVGAAPGAPAPGCISSQPGHTPHPAASRDPVART 69

QY 63 LPLO-PSSTMGOVGRQLAII-----GDDINRRYDSEFQTMLOHLOPTAENAYEY 110
DB 70 SPLQTPAAPGAAGPALSPPVPPVHLLTQAGDDFSRRYRGDFAEMSSQLHLTPFTARGR 129

QY 111 FTKIATSLFESGINWGRVALLGFGYRLALHVYQGLTGFLGQVTRFVVDFMLHHCIARW 170
DB 130 FATVVEELFRDGVNWGRIVAFPEFGVCMVEAVNREMSPLVDNIALWTEILNRH-LHTW 188

QY 171 IAORGWVAALNLGNLPI-----LNVLVVLGVLLG 201
DB 189 IQDNGGWDAFVEL-YGPSMRPLFDFSWLSLKTLLSLALVG 227
```

Search completed: December 6, 2004, 16:24:07
Job time : 142 secs

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RESULT 15
US-10-148-953A-4
; Sequence 4, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: modified Bcl-2 protein
US-10-148-953A-4
```

```
Query Match 17.4%; Score 192; DB 15; Length 239;
Best Local Similarity 26.4%; Pred. No. 1.7e-10;
Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;

QY 30 DTEVFRSYVYRHHQ---EQEAEGV-----AAPA-----DPEMVT 62
DB 10 DNRDIVMKYIHYKLSQRYEWDAGDVGAAPGAPAPGCISSQPGHTPHPAASRDPVART 69
```

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Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPGPRCEGCEPALPSASEEQVAQDTBEVFRSYVYVYRHQOEQAEGVAAPADPEM 60
DB 1 MASGCGPGPRCEGCEPALPSASEEQVAQDTBEVFRSYVYVYRHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFMHLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFMHLHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFPFKS 211
DB 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFPFKS 211

RESULT 2
AAR81451
ID AAR81451 standard; protein; 211 AA.
XX AC AAR81451;
DT 02-JUL-1996 (first entry)
DE Bcl-Y apoptosis-related protein.
XX KW Bcl-Y; apoptosis; cell proliferation; cell death; diagnosis; therapy.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 188..205
FT /label= C-terminal domain
FT /note= "putative membrane localisation sequence"
XX WO9605232-A1.
XX 22-FEB-1996.
XX 09-AUG-1995; 95WO-US010103.
XX 09-AUG-1994; 94US-00287427.
XX 11-OCT-1994; 94US-00321071.
XX (IMMU-) IMMUNOGEN INC.
XX Chittenden TD;
XX WPI; 1996-139648/14.
XX N-PSDB; AAT17375.
XX New isolated human Bcl-Y protein - used to develop prods. for treating disorders characterised by inappropriate cell proliferation or cell death.
XX Claim 3; Fig 4; 100pp; English.
XX Bcl-Y protein (AAR81451) is a member of the Bcl-2 family and can induce apoptosis in cells and function as a negative regulator of Bcl-2 function. Bcl-Y mRNA was detected in all human tumour cell lines examined and is also widely expressed in primary human tissues. It can be obtd. by expression of a full-length cDNA clone (AAT17375) in pref. mammalian host cells. Bcl-Y can be used to develop prods. for treating disorders associated with inappropriate cell proliferation or cell death, and to raise antibodies used for the diagnosis or monitoring of such disorders
XX Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGCGPGPRCEGCEPALPSASEEQVAQDTBEVFRSYVYVYRHQOEQAEGVAAPADPEM 60
DB 1 MASGCGPGPRCEGCEPALPSASEEQVAQDTBEVFRSYVYVYRHQOEQAEGVAAPADPEM 60
QY 61 VTLPQPSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFMHLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVYQHGLTGFLGQVTRFVVDVFMHLHHCIARWIAQRGWVAA 180
QY 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFPFKS 211
DB 181 LNLGNGPILNLVNLVGLGVLLGQFVVRFPFKS 211

RESULT 3
AAW03668
ID AAW03668 standard; protein; 211 AA.
XX AC AAW03668;
DT 22-FEB-1997 (first entry)
DE Bak protein.
XX KW Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus; BHRF1; fusion protein; epitope tag; drug screening; co-precipitation; ELISA; immuncassay; antibody; protein interactive trapping; virucide; antitumour; diagnostic.
XX OS Homo sapiens.
XX WO9633416-A1.
XX 24-OCT-1996.
XX 19-APR-1996; 96WO-US005639.
XX 20-APR-1995; 95US-00426529.
XX (LXRB-) LXR BIOTECHNOLOGY INC.
XX Barr PJ, Kiefer MC;
XX WPI; 1996-485886/48.
XX N-PSDB; AAT42138.
XX Screening for anti-viral agents - by detecting the ability of an agent to disrupt the interaction of a Bak protein and a viral protein.
XX Disclosure; Fig 1; 24pp; English.
XX This Bak protein sequence represents a bcl-1 homologue which interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is capable of modulating apoptosis. The protein may be used in complete or partial form, or as an epitope tag fusion protein, in a new virucide drug screening method, which involves combination of Bak protein and a viral protein (e.g. EBV BHRF1) exposure to a test compound, and monitoring for disruption of the interaction, e.g. by co-precipitation, protein interactive trapping or ELISA. Interaction of Bak and viral proteins allows viral replication or latency in the absence of apoptosis. Compounds which inhibit the interaction may be used as virucide, antitumour or diagnostic agents
XX Sequence 211 AA;

Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPRQEGCEGEPALPSAEEQVAQDTEEVFRSYVYRHOQOEAEAGVAAPADPEM 60
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 1 MASGGGPPRQEGCEGEPALPSAEEQVAQDTEEVFRSYVYRHOQOEAEAGVAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVALLGFGYRLALHVVYOHGLTGELGOVTRFVDFMLHHCIAEWIAQRGWVAA 180
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 121 SGINWGRVALLGFGYRLALHVVYOHGLTGELGOVTRFVDFMLHHCIAEWIAQRGWVAA 180

QY 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 4
AAW79534
ID AAW79534 standard; protein; 211 AA.
XX
AC AAW79534;
XX
DT 11-JAN-1999 (first entry)
XX
DE Bak polypeptide.
XX
KW Bak; bak binding protein; BBP; BPPD-1; BPPD-2; Bcl-2; apoptosis;
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

OS Homo sapiens.
XX
FH Key
FT Peptide
FT 103.126
FT /label= BPPD-1
FT /note= "Claim 36"
FT Peptide
FT 138.156
FT /label= BPPD-2
FT /note= "Claim 62"
XX
PN WO9841626-A1.
XX
PD 24-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004079.
XX
PR 20-MAR-1997; 97US-0041328P.
XX
PR 09-JAN-1998; 98US-0071097P.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Kiefer MC, Fitzpatrick PA, Gibson HL, Barr PV;
XX
WI 1998-521220/44.
XX
DR N-PSDB; AAV61498.
XX
PT New Bak-binding protein and related nucleic acid, vectors, transformed
Cc cells and antibodies - are useful for modulation of apoptosis in cancer,
Cc neuro-degeneration etc., also peptide fragments of Bak that interact with
Cc the protein.

PS Disclosure; Fig 2A-C; 77pp; English.
XX
CC This is the amino acid sequence of human Bak, a member of the Bcl-2
Cc family that is expressed in heart and other tissues, and which is capable
Cc of either killing cells, or actively protecting cells from apoptosis,
Cc depending on how it interacts with other cellular proteins. A nucleotide
Cc sequence (see AAV61498) encoding Bak is provided. The invention relates
Cc to a novel Bak binding protein (BBP, see AAW79537), the gene encoding BBP

(see AAV61499), methods for detecting substances that alter the specific
Cc binding between Bak and BBP, as well as diagnostic and therapeutic
Cc methods utilizing BBP. The invention also encompasses novel Bak-derived
Cc peptides, designated BBP binding domains (BBPBDs), and novel nucleotides,
Cc designated BBPBD-1 and BBPBD-2 encoding the peptides, which are involved
Cc in the interaction between Bak and BBP, and which have been characterised
Cc as important death domains of Bak. Modulation of the interaction between
Cc proteins that control apoptosis is a major focal point in the treatment
Cc of heart disease, viral infection and cancer

XX Sequence 211 AA;
SQ

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGGPPRQEGCEGEPALPSAEEQVAQDTEEVFRSYVYRHOQOEAEAGVAAPADPEM 60
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 1 MASGGGPPRQEGCEGEPALPSAEEQVAQDTEEVFRSYVYRHOQOEAEAGVAAPADPEM 60

QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSEFQTMQLQHPAENAYEYFTKIATSLFE 120

QY 121 SGINWGRVALLGFGYRLALHVVYOHGLTGELGOVTRFVDFMLHHCIAEWIAQRGWVAA 180
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 121 SGINWGRVALLGFGYRLALHVVYOHGLTGELGOVTRFVDFMLHHCIAEWIAQRGWVAA 180

QY 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Cc cell death; cancer; lymphoma; neurodegeneration; heart disease;
Cc cell proliferation; infection; human; therapy; diagnosis.

Db 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 5
AAW05433
ID AAW05433 standard; peptide; 211 AA.
XX
AC AAW05433;
XX
DT 02-JUL-1999 (first entry)
XX
DE Human BAK protein sequence.
XX
KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
Cc apoptosis promoter; cancer cell; virus infected cell; inflammation;
Cc autoantibody producing cell; cancer; lymphoproliferative condition;
Cc arthritis; autoimmune disease; therapy.

OS Homo sapiens.
XX
PN WO9916787-A1.
XX
PD 08-APR-1999.
XX
PF 22-SEP-1998; 98WO-US019765.
XX
PR 26-SEP-1997; 97US-0060133P.
XX
PR 07-OCT-1997; 97US-00946039.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
WI 1999-255058/21.
XX
PT Bcl homology domain 3 polypeptide.
XX
PS Disclosure; Fig 21b; 104pp; English.

CC This sequence represents the human BAK protein. The invention relates to
Cc a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member
Cc of the BCL-2 family. The BH3 polypeptide can be used in a method for
Cc promoting apoptosis in a target cell, especially where the cell is a

CC cancer cell a virus infected cell or an autoantibody producing cell. The
CC BH3 polypeptide can be used in therapeutic compositions for treating
CC disease including cancer, other lymphoproliferative conditions,
CC arthritis, inflammation, and autoimmune diseases, which may result from
CC the down regulation of cell death regulation
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFVSRYVYFHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFVSRYVYFHQOEAEAGVAAPADPEM 60
QY 61 VTLPQPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMQLQPTAENAYEYFTKIATSLPE 120
DB 61 VTLPQPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMQLQPTAENAYEYFTKIATSLPE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRCGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRCGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVWRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVWRFFKS 211

RESULT 6
ABB82374
ID ABB82374 standard; protein; 211 AA.
XX
AC ABB82374;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human BAK protein sequence.
XX
KW BAK; Mill; cytostatic; neuroprotective; neurotropic; cerebroprotective;
XX apoptosis; human.
XX
OS Homo sapiens.
XX
FN WO200274908-A2.
XX
PD 26-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US0006757.
XX
PR 02-MAR-2001; 2001US-0273091P.
XX
FA (MDSF-) MDS PROTEOMICS INC.
XX
PI Mcfadden G, Moran MF;
XX
PI WPI; 2002-740855/80.
XX
DR
XX
PT Identifying agents which may be potentially pro-apoptotic or anti-
XX apoptotic for treating acute and chronic neurodegenerative diseases,
XX comprises determining the effect of the test agent on complexes of BAK
XX and/or M1L1 proteins.
XX
PS Disclosure; Fig 11; 83pp; English.
XX

XX The invention relates to identifying agents which may be potentially pro-
XX -apoptotic or anti-apoptotic which involves determining the effect of a
XX test agent on the complexes of BAK and/or M1L1 proteins. The methods are
XX useful for identifying agents which may be potentially pro-apoptotic or
XX anti-apoptotic and for identifying M1L1-interacting polypeptides, and in
XX conducting a target or drug discovery system. The methods are useful for
XX identifying agents capable of inhibiting M1L1 activity or which can mimic
XX the activity of M1L1 by inhibiting the activity of BAK and which are

CC therefore anti-apoptotic agents. Agents identified by the method as
CC involved in regulation of apoptosis may be used in the development of
CC therapeutic agents and methods, and drug screening assays, and in
CC increasing the sensitivity of cancer cells to chemotherapeutic treatment.
CC Therapeutic applications of apoptosis manipulation include treatment of
CC acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or
CC Huntington's disease by drugs, and sensitization of cancer cells for drug
CC /radiation-induced apoptosis by modulation of survival signals and viral
CC transfer of apoptosis promoting genes. The present sequence represents a
CC human BAK protein
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFVSRYVYFHQOEAEAGVAAPADPEM 60
DB 1 MASGGGPPRQCGPAPLPSASEEQVADTEVFVSRYVYFHQOEAEAGVAAPADPEM 60
QY 61 VTLPQPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMQLQPTAENAYEYFTKIATSLPE 120
DB 61 VTLPQPSSSTMGGVGRQLAIIGDDINRRYDSBFQTMQLQPTAENAYEYFTKIATSLPE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRCGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRCGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVWRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVWRFFKS 211

RESULT 7
AAE37655
ID AAE37655 standard; protein; 211 AA.
XX
AC AAE37655;
XX
DT 27-AUG-2003 (first entry)
XX
DE Bcl2 related protein #6.
XX
KW Bcl2 related protein; growth; protein expression.
XX
OS Unidentified.
XX
FN WO2003040374-A1.
XX
PD 15-MAY-2003.
XX
PF 02-NOV-2001; 2001WO-US045553.
XX
PR 02-NOV-2001; 2001WO-US045553.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Lee C, Ly C, Moore G, Shi X;
XX
PI WPI; 2003-441576/41.
XX
PT New protein expression enhancing Bcl2 related nucleic acid for producing
XX commercially useful amounts of expressed protein, comprises a nucleic
XX acid that encodes an expressible protein or at least one Bcl2 related
XX protein.
XX
PS Disclosure; Page 52-53; 54pp; English.
XX
CC The invention relates to methods and compositions for enhanced protein
XX expression and/or growth of cultured cells using co-transcription of at
XX least one Bcl2 related protein encoding nucleic acid molecules. The
XX invention is useful in providing enhanced growth of and/or protein

CC production from cultured mammalian host cells used for the production of
CC commercially useful amounts of expressed protein. The present sequence is
CC Bcl2 related protein
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 6; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASCGGPPRQECGEPALPSASEEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60
DB 1 MASCGGPPRQECGEPALPSASEEQVAQDTEEVFRSVYFRHQEQEAGVAAAPADPEM 60
QY 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFQTMLOHQPDAENAYEYFTKIATSLFE 120
DB 61 VTLPQSSSTMVGQVGRQLAIGDDINRRYDSEFQTMLOHQPDAENAYEYFTKIATSLFE 120
QY 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWVAA 180
DB 121 SGINMGVALLGFGYRLALHYQHGLTGFLGQVTRFVDFMLHHCIAEWIAQGGWVAA 180
QY 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 8

ABR47397
ID ABR47397 standard; protein; 211 AA.

AC ABR47397;

XX 12-JUN-2003 (first entry)

DT Breast cancer associated protein sequence SEQ ID NO:25.

DE Human; breast cancer; cytostatic; gene therapy.

XX Homo sapiens.

XX WO2003004989-A2.

PN 16-JAN-2003.

XX 21-JUN-2002; 2002WO-US019669.

XX 21-JUN-2001; 2001US-0299887P.

PR 27-JUN-2001; 2001US-0301572P.

PR 18-JUL-2001; 2001US-0306501P.

PR 25-SEP-2001; 2001US-0325002P.

PR 05-MAR-2002; 2002US-0362585P.

PR 14-MAY-2002; 2002US-0380391P.

XX (MILL-) MILLENIUM PHARM INC.

PA Lillie J, Cannavarapu M, Glatk K, Hoersch S, Kamatkar S;

PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;

PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;

XX WPI; 2003-210381/20.

DR N-PSDB; ACC50088.

XX Breast cancer diagnosis or treatment by comparing the level of expression

PT of a marker in a patient sample with that in the control non-breast

PT cancer sample.

PT Claim 1; SEQ ID NO 25; 128pp; English.

PS The present invention describes a method for assessing whether a patient

XX is afflicted with breast cancer. The method comprises comparing the level

CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and

CC ABR47386 to ABR47632) in a patient sample and the normal level of

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CC combination of compounds; and (ii) assaying for a conformational change
CC in the Bak protein of the cells. The conformational change is preferably
CC determined at the N-terminus of Bak or in its BHI domain, particularly
CC using a specific binding partner, such as an antibody, for the
CC conformationally altered protein. Conformational change in Bak is a very
CC early (and general) indicator of commitment to apoptosis occurring
CC before caspase activation, nuclear condensation or cellular blebbing, and
CC is caused by agents that induce apoptosis by different mechanisms.
CC Detecting commitment to apoptosis is a more accurate indicator of
CC activity than cell death and the present method is quicker and simpler
CC than known clonogenic assays.

XX Sequence 211 AA;
SQ
Query Match 100.0%; Score 1103; DB 7; Length 211;
Best Local Similarity 100.0%; Pred. NO. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASGGGPPRQCGPAPLPASAEQVADTEVFRSYVYRHHQOEAGVAAAPADPEM 60
Db 1 MASGGGPPRQCGPAPLPASAEQVADTEVFRSYVYRHHQOEAGVAAAPADPEM 60
Qy 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPATENAYEYFTKIATSLFE 120
Db 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPATENAYEYFTKIATSLFE 120
Qy 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
Db 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
Qy 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Db 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 10
ADLF60830
ID ADF60830 standard; protein; 211 AA.
XX ADF60830;
XX ADF60830;
DT 12-FEB-2004 (first entry)
XX Human Bak #SEQ ID 1.
XX Chemotherapeutic; anti-apoptotic; Bak; Bcl-2; Bcl-XL; cancer; human.
XX Homo sapiens.
XX WO2003062829-A2.
XX 31-JUL-2003.
XX 17-JAN-2003; 2003WO-GB000185.
XX 17-JAN-2002; 2002GB-00000970.
XX (UYMA-) UNIV VICTORIA MANCHESTER.
XX Griffiths GJ;
XX WPI; 2003-902664/82.
XX Detecting or screening for chemotherapeutic activity, useful for treating
XX cancer, from induction of modifications in Bak protein in cells over
XX expressing anti-apoptotic protein.
XX Disclosure; Page 3; 32pp; English.
XX The invention relates to a method for detecting a chemotherapeutic
XX activity in a compound other than an etoposide, or in a combination of
XX compounds. In the method of the invention, a cell that over expresses an
XX anti-apoptotic protein is treated with at least one compound, and any

CC change in the conformation of cellular Bak, indicative of
CC chemotherapeutic activity, is detected. The anti-apoptotic protein is Bcl
CC -2 or Bcl-XL, and is over expressed by transfecting the cells with a
CC pcDNA3.1 vector that contains the anti-apoptotic-expressing sequence
CC under control of the cytomegalovirus promoter. The method of the
CC invention is used to identify, or screen for, chemotherapeutic agents for
CC the treatment of cancer. The current sequence represents the human Bak
CC amino acid sequence.

XX Sequence 211 AA;
SQ
Query Match 100.0%; Score 1103; DB 7; Length 211;
Best Local Similarity 100.0%; Pred. NO. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASGGGPPRQCGPAPLPASAEQVADTEVFRSYVYRHHQOEAGVAAAPADPEM 60
Db 1 MASGGGPPRQCGPAPLPASAEQVADTEVFRSYVYRHHQOEAGVAAAPADPEM 60
Qy 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPATENAYEYFTKIATSLFE 120
Db 61 VTLPQPSSTMGQVGRQLAIIIGDDINRRYDSFQTMQLHQPATENAYEYFTKIATSLFE 120
Qy 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
Db 121 SGINWGRVALLGFGYRLALHYVQHGLTGFLGQVTRFVVDVDFMLHHCIARWIAQRGWVAA 180
Qy 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211
Db 181 LNLGNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 11
ADLF69726
ID ADLF69726 standard; protein; 211 AA.
XX ADLF69726;
XX ADLF69726;
DT 20-MAY-2004 (first entry)
XX Human Bcl2 related protein #6.
XX Bcl2 related protein; therapeutic protein; human.
XX Homo sapiens.
XX US2004043028-A1.
XX 04-MAR-2004.
XX 02-NOV-2001; 2001US-00003632.
XX 02-NOV-2001; 2001US-00003632.
XX (LEEC/) LEE C.
XX (SHIX/) SHI X.
XX (LYCC/) LY C.
XX (MOOR/) MOORE G.
XX Lee C, Shi X, Ly C, Moore G;
XX WPI; 2004-225672/21.
XX New Bcl2 encoding nucleic acids for enhancing growth and/or production of
XX therapeutic or diagnostic proteins from cultured mammalian host cells.
XX Disclosure; SEQ ID NO 6; 42pp; English.
XX The invention relates to a protein expression enhancing Bcl2 related
XX nucleic acid comprising a first nucleic acid encoding at least one
XX expressible protein and a second nucleic acid encoding at least one Bcl2
XX related protein, where expression of the expressible protein is enhanced
XX by transcription or translation of the second nucleic acid. The

CC composition and methods are useful for enhancing growth and/or production
CC of therapeutic or diagnostic proteins from cultured mammalian host cells.
CC The present sequence is human Bcl2 related protein.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 8; Length 211;
Best Local Similarity 100.0%; Pred. NO. 1.4e-112;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MASQGGPPRQECGEPALPSASBEQVAQDTEEVFRSYVYRHQEQEAGVAAAPADPEM 60
DB 1 MASQGGPPRQECGEPALPSASBEQVAQDTEEVFRSYVYRHQEQEAGVAAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
DB 121 SGINWGRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 12

AAR77877
ID AAR77877 standard; protein; 211 AA.

XX AAR77877;
XX
XX 25-MAR-2003 (revised)
XX 21-NOV-1995 (first entry)
XX Human Cdn-2.
XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX autoimmune disease; reperfusion injury; hepatitis; osteoporosis; shock;
XX lymphoma; eczema.
XX Homo sapiens.

XX WO9515084-A1.

XX 08-JUN-1995.

XX 30-NOV-1994; 94WO-US013930.

XX 30-NOV-1993; 93US-00160067.

XX 07-OCT-1994; 94US-00320157.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Kiefer MC, Barr PJ;

XX WPI; 1995-215106/28.

XX N-PSDB; AAQ95493.

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
XX related vectors, transformed cells, proteins and antibodies, useful for
XX diagnosis and treatment e.g. of HIV infection, reperfusion injury etc.

XX Disclosure; Fig 5D-E; 66pp; English.

XX Cdn-2 cDNA was isolated from a human placental genomic library using a 950
XX bp fragment of Cdn-1 cDNA. Expression of Cdn-2 in mouse progenitor B-cell
XX FL5.12 cells decreased IL-3-induced apoptosis. The Cdn-2 protein
XX displayed 97% amino acid identity with Cdn-1 (AAR77876). (Updated on 25-
XX MAR-2003 to correct PN field.)

XX Sequence 211 AA;

Query Match 97.5%; Score 1075; DB 2; Length 211;
Best Local Similarity 97.2%; Pred. NO. 1.7e-109;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MASQGGPPRQECGEPALPSASBEQVAQDTEEVFRSYVYRHQEQEAGVAAAPADPEM 60
DB 1 MASQGGPPRQECGEPALPSASBEQVAQDTEEVFRSYVYRHQEQEAGVAAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIGDDINRRYDSEFQTMQLQLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
DB 121 SGINWGRVALLGFGYRLALHVYQHGLTGFLGQVTRFVDFMLHHCIARWIAQGGWVAA 180
QY 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211
DB 181 LNLNGPILNLVVLGVLLGQFVVRFFKS 211

RESULT 13

AAW03669
ID AAW03669 standard; protein; 211 AA.

XX AAW03669;

XX 22-FEB-1997 (first entry)

XX Bak-2 protein.

XX Human; Bak-2; apoptosis; latency; virus replication; Epstein-Barr virus;
XX BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
XX ELISA; immunoassay; antibody; protein interactive trapping; virucide;
XX antitumour; diagnostic.

XX Homo sapiens.

XX WO9633416-A1.

XX 24-OCT-1996.

XX 19-APR-1996; 96WO-US005639.

XX 20-APR-1995; 95US-00426529.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI; 1996-485886/48.

XX N-PSDB; AAT42139.

XX Screening for anti-viral agents - by detecting the ability of an agent to
XX disrupt the interaction of a Bak protein and a viral protein.

XX Disclosure; Fig 2; 24pp; English.

XX This Bak-2 protein sequence represents a bcl-1 homologue which interacts
XX with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein, and is
XX capable of modulating apoptosis. The protein may be used in complete or
XX partial form, or as an epitope tag fusion protein, in a new virucide drug
XX screening method, which involves combination of Bak-2 protein and a viral
XX protein (e.g. EBV BHRF1), exposure to a test compound, and monitoring for
XX disruption of the interaction, e.g. by co-precipitation, protein
XX interactive trapping or ELISA. Interaction of Bak-2 and viral proteins
XX allows viral replication or latency in the absence of apoptosis.
XX Compounds which inhibit the interaction may be used as virucide,
XX antitumour or diagnostic agents

XX Sequence 211 AA;

Query Match
Best Local Similarity 97.5%; Score 1075; DB 2; Length 211;
Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASGGGPPRQCEGEPALPSASEBQVADTEEVRSVYFVHQQEQAEGVAAPADPEM 60
DB 1 MASGGGPPRQCEGEPALPSASEBQVADTEEVRSVYFVHQQEQAEGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
QY 181 LNLGSPILNLVLGVLGQVVRFFPKS 211
DB 181 LNLGSPILNLVLGVLGQVVRFFPKS 211

RESULT 14
ADP04114
ID ADP04114 standard; protein; 211 AA.
XX AC ADP04114;
XX DT 09-SEP-2004 (first entry)
XX DE Human colon specific protein SEQ ID NO:95.
XX DE human; colon specific nucleic acid; CSNA; colon specific protein; CSP;
XX KW cytostatic; vaccine; gene therapy; colon cancer.
XX OS Homo sapiens.
XX PN WO2004050858-A2.
XX PD 17-JUN-2004.
XX PF 04-DEC-2003; 2003WO-US038808.
XX PR 04-DEC-2002; 2002US-0431133P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Macina RA, Turner LR, Sun Y, Rodriguez M, Burcham TS;
XX WPI; 2004-480622/45.
XX DR Novel colon specific protein derived from normal and neoplastic colon
XX cell, useful as vaccine in treating colon cancer and in identifying,
XX diagnosing, monitoring, staging, imaging colon cancer and non-cancerous
XX disease state in colon.
XX FS Claim 12; SEQ ID NO 95; 655pp; English.
XX CC The invention relates to a novel colon specific protein (CSP) (I), and
XX the nucleic acid encoding it. A CSP of the invention has cytostatic
XX activity, and may have use in a vaccine, and in gene therapy. The CSP is
XX useful for determining the presence of a colon specific protein in a
XX sample. The nucleic acid encoding the CSP is useful for determining the
XX presence of a colon specific nucleic acid (CSNA) in a sample. The CSP and
XX CSNA are useful for diagnosing or monitoring the presence and metastases
XX of colon cancer in a patient. The method of administering a composition
XX comprising a CSP or CSNA is useful for treating a patient with colon
XX cancer. The CSP and CSNA are useful as vaccine for treating colon cancer
XX and non-cancerous disease states in colon. The present sequence
XX represents a CSP of the invention.
XX SQ Sequence 211 AA;
Query Match
Best Local Similarity 85.8%; Score 946; DB 8; Length 211;

Best Local Similarity 97.8%; Pred. No. 2.7e-95;
Matches 179; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MASGGGPPRQCEGEPALPSASEBQVADTEEVRSVYFVHQQEQAEGVAAPADPEM 60
DB 1 MASGGGPPRQCEGEPALPSASEBQVADTEEVRSVYFVHQQEQAEGVAAPADPEM 60
QY 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
DB 61 VTLPQPSSTMGQVGRQLAIIGDDINRRYDSFQTMLOHLOPTAENAYEYFTKIATSLFE 120
QY 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVAA 180
DB 121 SGINWGRVVALLGFGYRLALHYVQHGLTGFLGQVTRFVDFMLHHCIARWIAQRGWVSI 180
QY 181 LNL 183
DB 181 QGL 183

RESULT 15
RAY05432
ID AAY05432 standard; peptide; 208 AA.
XX AC AAY05432;
XX DT 02-JUL-1999 (first entry)
XX DE Mouse BAK protein sequence.
XX KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
XX apoptosis promoter; cancer cell; virus infected cell; inflammation;
XX autoantibody producing cell; cancer; lymphoproliferative condition;
XX arthritis; autoimmune disease; therapy.
XX OS Mus sp.
XX PN WO9916787-A1.
XX PD 08-APR-1999.
XX PF 22-SEP-1998; 98WO-US019765.
XX PR 26-SEP-1997; 97US-0060133P.
XX PR 07-OCT-1997; 97US-00946039.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX WPI; 1999-255059/21.
XX DR Bcl homology domain 3 polypeptide.
XX PT Disclosure; Fig 21b; 104pp; English.
XX FS This sequence represents the murine BAK protein. The invention relates to
XX a bcl homology domain 3 (BH3 domain), derived from a proapoptotic member
XX of the BCL-2 family. The BH3 polypeptide can be used in a method for
XX promoting apoptosis in a target cell, especially where the cell is a
XX cancer cell a virus infected cell or an autoantibody producing cell. The
XX BH3 polypeptide can be used in therapeutic compositions for treating
XX disease including cancer, other lymphoproliferative conditions,
XX arthritis, inflammation, and autoimmune diseases, which may result from
XX the down regulation of cell death regulation
XX Sequence 208 AA;
Query Match
Best Local Similarity 75.2%; Score 829.5; DB 2; Length 208;
Matches 161; Conservative 20; Mismatches 27; Indels 3; Gaps 2;

QY 1 MASGGGPPRQCEGEPALPSASEBQVADTEEVRSVYFVHQQEQAEGVAAPADPEM 60

Db	1	MASQGGPPKVGCDSE--PSPSEQVAQDTEEVFRSYVYLHQEQETQG-RPPANPEM	57
Qy	61	VTLEPQFSSTWQVGRQALIGDDINRRYDSEFQTMLOHLOPTAENAYEYFTKIATSLFE	120
Db	58	DNLSLEFNSILGQVGRQALIGDDINRRYDTEFQNLLEQLQPTAGNAYELFTKIASSLPK	117
Qy	121	SGINWGRVALLGFGYELALHVVYQHGLTGFLGOVTRFVVDFMLHHCIARWIAORGWVAA	180
Db	118	SGISWGRVALLGFGYELALYVYQGLTGFLGQVTCFLADIILHHYIARWIAORGWVAA	177
Qy	181	LNLGNGFILNVVLGVLLGQFVVRFPKS	211
Db	178	LNLRDPILTVMVIFGVLLGQFVVRFPKS	208

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